

once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C46F11 is at 45409 in sequence Z48241.

The true right end of clone C46F11 is at 8174 in sequence Z48245.

The start of this sequence (1..102) overlaps with the end of sequence Z48241.

The end of this sequence (34740..34841) overlaps with the start of sequence Z48245.

FEATURES Location/Qualifiers
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1081 ctggtagagc aggaaatcg ggtactgctt atacatttt cacacccgac gaagagagat
1141 tctttcgtc aatcattaaa gcttggaaac aatctggttc aaaagtaccc gatgaactta
1201 gaaaattgaa tgatacctac gagaaaaaga gaaaagaagg taaggatgtatc tattggcac
1261 caaccggttt cactggtaga ggtcataat ttgatgctgc cgaagaggat aaaaagaata
1321 ttgaaagaaa acaacaaga aaagcatatg gtatcgaaga ggaagaagaa gaagaggatg
1381 aagataaaga aaaagctgaa aaggagaaat tggccgctgc ttccgctgaa aaagaaaaac
1441 aattattatc tgaaaaagaa aaattggatc ctgctaccac taatactatc gtcataacctg
1501 gtgttagatgg tacaatcatt acaccttctt cattacttca aaccgatctt tcagttctg
1561 tggcaaca ggctatcaat caaatatttg gtatccaca agttacctcc tccgaagaag
1621 caattaaaaa acttcaattt gcccgtcaat taggtatgaa aggtatatt caaaaattaa
1681 ataatcaaat aactccattt aatcaaactc atttcatttca agaatttagaa attaatgatt
1741 cggaattc

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1: P09052[gi:1352826] This record was replaced or removed. See [revision history](#) for details.

LOCUS P09052 661 aa linear INV 01-FEB-1996

DEFINITION VASA PROTEIN.

ACCESSION P09052

VERSION P09052 GI:1352826

DBSOURCE swissprot: locus VASA_DROME, accession P09052;

class: standard.

created: Nov 1, 1988.

sequence updated: Feb 1, 1996.

annotation updated: Feb 1, 1996.

xrefs: gi: [433675](#), gi: [1054723](#), gi: [8804](#), gi: [84895](#), gi: [84894](#)

xrefs (non-sequence databases): FLYBASEFBgn0003970, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS Developmental protein; ATP-binding; Repeat; Helicase.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydriidea; Drosophilidae; Drosophila.

REFERENCE 1 (residues 1 to 661)

AUTHORS Lasko, P.F. and Ashburner, M.

TITLE The product of the Drosophila gene vasa is very similar to eukaryotic initiation factor-4A

JOURNAL Nature 335 (6191), 611-617 (1988)

MEDLINE [89014721](#)

REMARK SEQUENCE FROM N.A.

REFERENCE 2 (residues 1 to 661)

AUTHORS LASKO, P.F.

TITLE Direct Submission

JOURNAL Submitted (~DEC-1993)

REMARK REVISIONS.

REFERENCE 3 (residues 1 to 661)

AUTHORS Hay, B., Jan, L.Y. and Jan, Y.N.

TITLE A protein component of Drosophila polar granules is encoded by vasa and has extensive sequence similarity to ATP-dependent helicases

JOURNAL Cell 55 (4), 577-587 (1988)

MEDLINE [89028669](#)

REMARK SEQUENCE FROM N.A.

COMMENT [WARNING] On Feb 1, 2001 this sequence was replaced by a newer version gi:[12644110](#).

On Jun 4, 1996 this sequence version replaced gi:[137452](#).

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The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] THE VASA PROTEIN IS REQUIRED ONLY IN THE FEMALE GERM LINE. IT IS IMPORTANT FOR OOCYTE FORMATION AND IN THE SPECIFICATION OF THE POSTERIOR STRUCTURES OF THE EMBRYO.

[DEVELOPMENTAL STAGE] MATERNALLY EXPRESSED (DURING OOGENESIS). FUNCTION DURING EARLY EMBRYOGENESIS.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES.

FEATURES Location/Qualifiers

source 1..661
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"

gene 1..661
/gene="VAS"

Protein 1..661
/gene="VAS"
/product="VASA PROTEIN"

Region 35
/gene="VAS"
/region_name="Conflict"
/note="A -> R (IN REF. 3)."

Region 93..127
/gene="VAS"
/region_name="Domain"
/note="5 X 7 AA TANDEM REPEATS OF [FS]-R-G-G- [EQ]-G-G."

Region 93..99
/gene="VAS"
/region_name="Repetitive region"
/note="1."

Region 100..106
/gene="VAS"
/region_name="Repetitive region"
/note="2."

Region 107..113
/gene="VAS"
/region_name="Repetitive region"
/note="3."

Region 114..120
/gene="VAS"
/region_name="Repetitive region"
/note="4."

Region 121..127
/gene="VAS"
/region_name="Repetitive region"
/note="5."

Region 265
/gene="VAS"
/region_name="Conflict"
/note="F -> Y (IN REF. 3)."

Site 289..296
/gene="VAS"
/site_type="np-binding"
/note="ATP (BY SIMILARITY)."

Site 399..402
/gene="VAS"
/site_type="unclassified"
/note="DEAD BOX."

Region 582
/gene="VAS"
/region_name="Conflict"
/note="C -> R (IN REF. 3)."

Region 594
/gene="VAS"
/region_name="Conflict"
/note="D -> H (IN REF. 3)."

Region 644
/gene="VAS"
/region_name="Conflict"
/note="R -> RQ (IN REF. 3)."

ORIGIN

1 msddwddepi vdtrgarggd wsddedtaks fsgeaedgv ggsggegggy qggndrvfgr
61 iggrggag gyrggnrdgg gfhggrrege rdfrggeggf rggqggsrgg qggssrgqgg
121 frgeggfrg rlyenedgde rrgrldreer ggerrgrldr eerggerger gdggfarrrr
181 neddinnnnn iaedverkre fyippepsnd aieifssgia sghfskynn ipvkvtgsdv
241 pqpiqhftsa dlrddiidnv nksgfkptp iqkcsipvis sgrdlmacaq tgsgktaafl
301 lpilsklled phelelgrpq vvivsptrel aiqifneark fafesylkig ivyggttsfrh
361 qnecitrgch vviatpgrll dfvdrtfitf edtrfvvlde adrmldmgsf edmrrimthv
421 tmrpehqqlm fsatfpeeq rmageflkny vsvaigivgg acsdvkqtly evnkyakrsk
481 lieilseqad gtivfvetkr gadflasfls ekefptsih gdrlqsreq alrdfkngsm
541 kvliatsvas rgldiknikh vinydmpski ddyvhright gcvgnngrat sffdpekdra
601 iaadlvkile gsgqtvpdf1 rtcgaggdgg ysnqnfggvd vrgrgnvygd atnveeeeqw
661 d

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1: Q64060. DEAD-box protein ...[gi:2500526]

LOCUS Q64060 713 aa linear ROD 01-NOV-1997

DEFINITION DEAD BOX PROTEIN 4 (VASA HOMOLOG) (RVLG).

ACCESSION Q64060

VERSION Q64060 GI:2500526

DBSOURCE swissprot: locus DDX4_RAT, accession Q64060;

class: standard.

created: Nov 1, 1997.

sequence updated: Nov 1, 1997.

annotation updated: Nov 1, 1997.

xrefs: gi: [806463](#), gi: [806464](#)

xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,

PROSITEPS00039

KEYWORDS ATP-binding; Helicase; RNA-binding.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (residues 1 to 713)

AUTHORS Komiya, T. and Tanigawa, Y.

TITLE Cloning of a gene of the DEAD box protein family which is specifically expressed in germ cells in rats

JOURNAL Biochem. Biophys. Res. Commun. 207 (1), 405-410 (1995)

MEDLINE 95160706

REMARK SEQUENCE FROM N.A.

STRAIN=WISTAR; TISSUE=TESTIS

COMMENT -----

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[TISSUE SPECIFICITY] TESTIS.
 [SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. HIGHEST TO DROSOPHILA VASA.

FEATURES Location/Qualifiers

source 1..713

/organism="Rattus norvegicus"
 /db_xref="taxon:10116"

gene 1..713

/gene="DDX4"

Protein 1..713

/gene="DDX4"

/product="DEAD BOX PROTEIN 4"

Site 317..324

/gene="DDX4"
 /site_type="np-binding"
 /note="ATP (POTENTIAL)."

Site 431..434

/gene="DDX4"
 /site_type="unclassified"
 /note="DEAD BOX."

ORIGIN

1 mgdedweaei lkphvssyvp vfekdkyssg angdtfnrts asssemedgp sgrdhfmrsg
61 fssgrnlgnr digesskret tstdggfgrg kgfgnrgfln nkfeegdssg fwkestndce
121 dtqtrsrgfs krggypdngd seasgpfrg grdseydqdg gsqrqggglfg srkpaasdsg
181 sgdtfqsrsg nargaykln eevvtgsgkn swkseaegge ssdiqgpktv yipppppede
241 dsifahyqtg infdkydtl vevsghdapp ailtfeeaml cqtlnnniak agytkltpvq
301 kysipivlag rdltmacaqtg sgktaafllp ilahmmrdgi tasrfkelqe peciivaptr
361 elinqiylea rkfsfgtcvr avviygtqf ghsirqvqg cnilcatpgr lmdiigkeki
421 glkqvkylvl deadrmlldmg fgpemkklis cpqmpskeqr qtllfsatfp eeiqlagef
481 lksnlyfvav gqvggacrdv qqsilqvgpv fkkrklveil rniqderpmv fvetkkadaf
541 iatflcqeki sttsihgdre qrereqalgd frcgkcpvlv atsvaargld ienvqhvinf
601 nlpstideyv hrigrtrgrcg ntgraisffd tesdnhraqp lvkvlslaqq dvpawleeia
661 fssyappsfs nstrgavfas fdtrknfqgk ntln>tagiss aqapnpvdde swd

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Features

 1: Q61496[gi:2500525] This record was replaced or removed. See [revision history](#) for details.

LOCUS Q61496 637 aa linear ROD 01-NOV-1997

DEFINITION DEAD BOX PROTEIN 4 (VASA HOMOLOG) (MVH).

ACCESSION Q61496

VERSION Q61496 GI:2500525

DBSOURCE swissprot: locus DDX4_MOUSE, accession Q61496;

class: standard.

created: Nov 1, 1997.

sequence updated: Nov 1, 1997.

annotation updated: Nov 1, 1997.

xrefs: gi: [286074](#), gi: [286075](#)

xrefs (non-sequence databases): MGI102670, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS ATP-binding; Helicase; RNA-binding.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (residues 1 to 637)

AUTHORS Fujiwara, Y., Komiya, T., Kawabata, H., Sato, M., Fujimoto, H., Furusawa, M. and Noce, T.

TITLE Isolation of a DEAD-family protein gene that encodes a murine homolog of *Drosophila* vasa and its specific expression in germ cell lineage

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12258-12262 (1994)

MEDLINE [95083681](#)

REMARK SEQUENCE FROM N.A.

STRAIN=BALB/C; TISSUE=TESTIS

COMMENT

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[SUBCELLULAR LOCATION] CYTOPLASMIC AND PERINUCLEAR.

[TISSUE SPECIFICITY] TESTIS.

[DEVELOPMENTAL STAGE] EXPRESSED IN SPERMATOGENIC CELLS FROM THE SPERMATOCYTE STAGE TO THE ROUND SPERMATID STAGE.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. HIGHEST TO DROSOPHILA VASA.

FEATURES Location/Qualifiers

source 1..637

/organism="Mus musculus"
/db_xref="taxon:10090"

gene 1..637

/gene="DDX4"
/note="synonym: MVH"

Protein <1..637

/gene="DDX4"
/product="DEAD BOX PROTEIN 4"
246..253
/gene="DDX4"

Site

Site
/site_type="np-binding"
/note="ATP (BY SIMILARITY)."
360..363
/gene="DDX4"
/site_type="unclassified"
/note="DEAD BOX."

ORIGIN

1 fgrgkfggnr gflnnkfeeg dssgfwkesn ndcednqtrs rgfskruggcq dgndseasgp
61 frrggrrgsfr gcrggffglgr pnsestdqdqg tqcgggflvl gkpaasdsgn gdtyqsrsgs
121 grggykglne evvtgsgkns wksetegges sdsqqpkvty ippppeded sifahyqtgi
181 nfdkydtilv evsghdappa iltfeeanc qtlnnnirka gytkltpvqk ytipivlagr
241 dlmacaqtgs gktaaffpi lahmmrdgit asrfkelqep eciivaptre linqiylear
301 kfsfgtcvis vviyggfqfg hsrqivqgc nilcatpgrl mdiigkekig lkqvkylvld
361 eadsmlmdmgf apeikkilisc pgmpskeqhq tllfsatfpe eiqrlagdfi ksnylfvavg
421 qvggacrdvq qtilqvgqyy keksllrfye nigdertmvf vetkkkadfi atflcqekis
481 stsihgreq rereqalgdf rcgkcpvlva tsvaargldi envqhvinfd lpstideyvh
541 rigrtgrcgn tgraissffdt dsdnhlaqpl vkvlndaqqd vpawleeiaf styvppsfss
601 strggavfas vdtrknyqgk ahveysgdff ftssqss

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Features

1: Q62167. DEAD-box protein ...[gi:2500528]

BLink, Domains, Links

LOCUS Q62167 662 aa linear ROD 15-JUL-1999

DEFINITION DEAD BOX PROTEIN 3 (DEAD-BOX RNA HELICASE DEAD3) (MDEAD3)
(EMBRYONIC RNA HELICASE) (D1PAS1 RELATED SEQUENCE 2).

ACCESSION Q62167

VERSION Q62167 GI:2500528

DBSOURCE swissprot: locus DDX3_MOUSE, accession Q62167;

class: standard.

extra accessions:O09060,O09143,created: Nov 1, 1997.

sequence updated: Nov 1, 1997.

annotation updated: Jul 15, 1999.

xrefs: gi: 1835121, gi: 1835122, gi: 407995, gi: 407996

xrefs (non-sequence databases): MGI103064, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (residues 1 to 662)

REFERENCE AUTHORS Sowden,J., Putt,W., Morrison,K., Beddington,R. and Edwards,Y.

TITLE The embryonic RNA helicase gene (ERH): a new member of the DEAD box family of RNA helicases

JOURNAL Biochem. J. 308 (Pt 3), 839-846 (1995)

MEDLINE 97104282

REMARK SEQUENCE FROM N.A.

STRAIN=C57BL/6, AND DBA

2 (residues 1 to 662)

REFERENCE AUTHORS Gee,S.L. and Conboy,J.G.

TITLE Mouse erythroid cells express multiple putative RNA helicase genes exhibiting high sequence conservation from yeast to mammals

JOURNAL Gene 140 (2), 171-177 (1994)

MEDLINE 94192995

REMARK SEQUENCE FROM N.A.

TISSUE=ERYTHROLEUKEMIA

COMMENT -----

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The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. IT MAY PLAY A ROLE IN TRANSLATIONAL ACTIVATION OF mRNA IN THE OOCYTE AND EARLY EMBRYO.

[TISSUE SPECIFICITY] DEVELOPMENTALLY REGULATED.

[DEVELOPMENTAL STAGE] EXPRESSED IN OOCYTES. UBIQUITOUSLY FOUND IN 9 DAYS POST-CONCEPTION EMBRYO, AT LATER STAGES IT IS RESTRICTED TO BRAIN AND KIDNEY.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers
source 1..662
/organism="Mus musculus"

gene /db_xref="taxon:10090"
1..662
/gene="DDX3"
/note="synonyms: DEAD3, ERH, D1PAS1-RS2"
Protein 1..662
/gene="DDX3"
/product="DEAD BOX PROTEIN 3"
Site 224..231
/gene="DDX3"
/site_type="np-binding"
/note="ATP (POTENTIAL)."
Site 347..350
/gene="DDX3"
/site_type="unclassified"
/note="DEAD BOX."
Region 582..662
/gene="DDX3"
/region_name="Domain"
/note="GLY/SER-RICH."
Region 609..616
/gene="DDX3"
/region_name="Domain"
/note="POLY-SER."
Region 624..630
/gene="DDX3"
/region_name="Domain"
/note="POLY-GLY."
Region 633..641
/gene="DDX3"
/region_name="Domain"
/note="POLY-GLY."
ORIGIN

1 mshvavenal gldqqfagld lnssdnqsgg staskgryip phlrnreatk gfydkdssgw
61 ssskdkdays sfgsrgdsrg kssffgdargs gsrgrfddrg rgdydgiggr gdrsfgfkfe
121 rggnsrwcdk sdeddwskpl ppsrleqel fsggntginf ekyddipvea tgnnccphie
181 sfsvemgei imgnieltry trptpvqkha ipiikekrdl macaqtgsgk taafllpils
241 qiyadgpgea lramkengry grkqypisl vlaptrelav qiyeearkfs yrsrvrvcvv
301 yggaeigqqi rdlergchll vatpgrlvdm mergkigldf ckyvlvdead rmlldmgfepq
361 irriiveqdtm ppkgvrhtmm fsatfpkeiq mlardfldey iflavgrvgts tsenitqkvv
421 wveeidkrssf lldllnatgk dsitlvfvet kkgadsledf lyhegyacts ihgdrsqrdr
481 eealhqfrsq kspilvatav aargldisnv khvinfdlps dieeyvhrieg rtgrvgnlql
541 atsffnerni nitkdlldll veakqevpsw lenmafehy kgssrgrsks srfsgggfgar
601 dyrqssgass ssfsssrass srsgggghgg srgfgggyg gfynsdgygg nynsqgvdw
661 gn

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Features

 1: O00571. DEAD-box protein ...[gi:3023628]

BLink, Domains, Links

JOCUS O00571 662 aa linear PRI 15-JUL-1999
DEFINITION DEAD BOX PROTEIN 3 (HELICASE-LIKE PROTEIN 2) (HLP2) (DEAD BOX, X ISOFORM).

ACCESSION O00571

VERSION 000571 GI:3023628

DBSOURCE swissprot: locus DDX3_HUMAN, accession O00571;

class: standard.

extra accessions:O15536,created: Jul 15, 1998.

sequence updated: Jul 15, 1998.

annotation updated: Jul 15, 1999.

xrefs: gi: [2148923](#), gi: [2148924](#), gi: [3523149](#), gi: [3523150](#), gi: [2580551](#), gi: [2580552](#), gi: [2580549](#), gi: [2580550](#)xrefs (non-sequence databases): MIM [300160](#), PFAMPF00270, PFAMPF00271, PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding.

SOURCE Homo sapiens (human)

ORGANISM [Homo sapiens](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 662)

AUTHORS CHUNG,J., LEE,S.-G. and SONG,K.

TITLE Identification of a human homolog of a putative RNA helicase gene (mDEAD3) expressed in mouse erythroid cells

JOURNAL Korean J. Biochem. 27, 193-197 (1995)

REMARK SEQUENCE FROM N.A.

TISSUE=LIVER, AND HIPPOCAMPUS

REFERENCE 2 (residues 1 to 662)

AUTHORS OWSIANKA,A.M. and PATEL,A.H.

TITLE Direct Submission

JOURNAL Submitted (~APR-1998)

REMARK SEQUENCE FROM N.A.

REFERENCE 3 (residues 1 to 662)

AUTHORS Lahm,B.T. and Page,D.C.

TITLE Functional coherence of the human Y chromosome

JOURNAL Science 278 (5338), 675-680 (1997)

MEDLINE [98022381](#)

REMARK SEQUENCE FROM N.A.

COMMENT -----

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[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. INTERACTS SPECIFICALLY WITH HEPATITIS C VIRUS CORE PROTEIN RESULTING A CHANGE IN INTRACELLULAR LOCATION.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source

1..662
/organism="Homo sapiens"

gene /db_xref="taxon:9606"
1..662
/gene="DDX3"
/note="synonym: DBX"
Protein 1..662
/gene="DDX3"
/product="DEAD BOX PROTEIN 3"
Region 50
/gene="DDX3"
/region_name="Conflict"
/note="K -> R (IN REF. 3)."
Site 224..231
/gene="DDX3"
/site_type="np-binding"
/note="ATP (POTENTIAL)."
Site 347..350
/gene="DDX3"
/site_type="unclassified"
/note="DEAD BOX."
Region 582..662
/gene="DDX3"
/region_name="Domain"
/note="GLY/SER-RICH."

ORIGIN

1 mshvavenal gldqqfafqld lnssdnqsgg staskgryip phlrnreatk gfydkdssgw
61 ssskdkdays sfgsrsdsrg kssffsdrgs qsrgrfddrq rsdydgigsr gdrsgfgkfe
121 rggnsrwcdk sdeddwspl ppserleqel fsggntginf ekyddipvea tgnncphie
181 fsfsdvmgei imgnieltry trptpvqkha ipiikekrdl macaqtgsgk taafllpils
241 qiysdgpgea lramkengry grrkqypisl vlaptrelav qiyeearkfs yrsrvrpcvv
301 yggadigqqi rdlergchll vatpgrlvdmergkigldf ckyvlvdead rmldmgfepq
361 irriiveqdttm ppkgvrhmm fsatfpkeiq mlardfldey iflavgrvgs tsenitqkv
421 wveesdkrsf lldllnatgk dsltlvfvet kkgadsledf lyhegyacts ihgdrsqrdr
481 eealhqfrsg kspilvatav aargldisnv khvinfdlps dieeyvhrieg rtgrvgnlgl
541 atsffnerni nitkdlldll veakqevpsw lenmayehhy kgssrgrsks srfsgggfar
601 dyrqssgass ssfsssrass srsgggghgs srgfgggyg gfynsdgygg nynsqgvdw
661 gn

//

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Features

BLink, Domains, Links

1: P24346. Putative ATP-depe...[gi:113825]

LOCUS P24346 697 aa linear VRT 01-FEB-1996

DEFINITION PUTATIVE ATP-DEPENDENT RNA HELICASE AN3.

ACCESSION P24346

VERSION P24346 GI:113825

DBSOURCE swissprot: locus AN3_XENLA, accession P24346;

class: standard.

created: Mar 1, 1992.

sequence updated: Mar 1, 1992.

annotation updated: Feb 1, 1996.

xrefs: gi: 65059, gi: 65060, gi: 103989, gi: 345587

xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,

PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopus.

REFERENCE 1 (residues 1 to 697)

AUTHORS Gururajan, R., Perry-O'Keefe, H., Melton, D.A. and Weeks, D.L.

TITLE The Xenopus localized messenger RNA An3 may encode an ATP-dependent RNA helicase

JOURNAL Nature 349 (6311), 717-719 (1991)

MEDLINE 91141586

REMARK SEQUENCE FROM N.A.

COMMENT -----
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The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source 1..697

/organism="Xenopus laevis"
/db_xref="taxon:8355"

gene 1..697

/gene="AN3"

Protein 1..697

/gene="AN3"

/product="PUTATIVE ATP-DEPENDENT RNA HELICASE AN3"

Site 265..272

/gene="AN3"
/site_type="np-binding"
/note="ATP (BY SIMILARITY)."
388..391
/gene="AN3"
/site_type="unclassified"
/note="DEAD BOX."

Region 623..697
/gene="AN3"
/region_name="Domain"
/note="GLY/SER-RICH."

ORIGIN

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301 ygrrkqfppls lvlaptrela vqiyeearkf ayrsrvrpcv vyggadigqq irdlergchl
361 lvatpgrlvd mm ergkigld fckylvldea drmldmgfep qirriveqdt mppkgvrqtm
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481 kdsltlvfve tkkgadaled flyhegyact sihgdrsqrds reealhqfrs gkspilvata
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601 lveakqevps wlenmayeqh hksssrgsrsk srfsgggfak dyrqssgags sfgssrggrs
661 sghggsrgfg ggyggfynsd gyggnyggss qvdwwgn

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Features

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P16381: Putative ATP-depe...[gi:130256]

LOCUS P16381 660 aa linear ROD 15-JUL-1999

DEFINITION PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.

ACCESSION P16381

VERSION P16381 GI:130256

DBSOURCE swissprot: locus PL10_MOUSE, accession P16381; class: standard.

created: Aug 1, 1990.

sequence updated: Aug 1, 1990.

annotation updated: Jul 15, 1999.

xrefs: gi: 200388, gi: 200389, gi: 110038

xrefs (non-sequence databases): PFAMPF00270, PFAMPF00271,

PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding; Spermatogenesis.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (residues 1 to 660)

REFERENCE AUTHORS Leroy, P., Alzari, P., Sasoon, D., Wolgemuth, D. and Fellous, M.

TITLE The protein encoded by a murine male germ cell-specific transcript is a putative ATP-dependent RNA helicase

JOURNAL Cell 57 (4), 549-559 (1989)

MEDLINE 89249320

REMARK SEQUENCE FROM N.A.

TISSUE=TESTIS

COMMENT -----

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[FUNCTION] PUTATIVE ATP-DEPENDENT RNA HELICASE. POSSIBLE ROLE IN A KEY STEP OF THE SPERMATOGENIC PROCESS.

[TISSUE SPECIFICITY] TESTIS.

[DEVELOPMENTAL STAGE] HIGH LEVELS OF PL10 DURING THE MEIOTIC AND HAPLOID STAGES OF SPERMATOGENESIS.

[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source 1..660

/organism="Mus musculus"
/db_xref="taxon:10090"

gene 1..660

/gene="PL10"
/note="synonym: D1PAS1"

Protein 1..660

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/product="PUTATIVE ATP-DEPENDENT RNA HELICASE PL10"
223..230
/gene="PL10"
/site_type="np-binding"

Site /note="ATP (POTENTIAL)." 346..349 /gene="PL10" /site_type="unclassified" /note="DEAD BOX."
Site 495..514 /gene="PL10" /site_type="DNA binding" /note="POTENTIAL."
Region 581..660 /gene="PL10" /region_name="Domain" /note="GLY/SER-RICH."
ORIGIN
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61 skdkdayssf gsrstdtraks sffsdrgggsg srgrfdergr sdyesvgsrg grsgfgkfer
121 ggnswcdka deddwskplp pserleqelf sggnntginfe kyddipveat gnnccpphies
181 fsdvemgeii mgnieltryt rptpvqkhai piikekrdlm acaqtgsgkt aafllpilsq
241 iytdgpgeal ramkengkyg rrkqgypislv laptrrelavq iyeearkf sy rsrvrpcvvy
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421 veeadkrsfl ldllnatgkd slilvfvetk kgadsledfl yhegyactsi hgdrsqrdr
481 ealhqfrsgk spilvatava argldisnvk hvinfldpsd ieeyvhigr tgrvgnlgla
541 tsffnernin itkdlldllv eakqevpswl enmafehyk ggsrgrsksr fsgggfardy
601 rqssgassss fssgrasnsr sgggshgssr gfgggsyggf ynsdgyggny ssqgvdwgn
//

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Features

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 1: O15523. DEAD-box protein ...[gi:6014945]

LOCUS O15523 660 aa linear PRI 15-JUL-1999

DEFINITION DEAD BOX PROTEIN 3, Y-CHROMOSOMAL.

ACCESSION O15523

VERSION O15523 GI:6014945

DBSOURCE swissprot: locus DDXY_HUMAN, accession O15523;

class: standard.

created: Jul 15, 1999.

sequence updated: Jul 15, 1999.

annotation updated: Jul 15, 1999.

xrefs: gi: 2580555, gi: 2580556, gi: 2580553, gi: 2580554

xrefs (non-sequence databases): MIM 400010, PFAMPF00270,

PFAMPF00271, PROSITEPS00039

KEYWORDS Helicase; ATP-binding; RNA-binding; DNA-binding.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 660)

AUTHORS Lahn, B.T. and Page, D.C.

TITLE Functional coherence of the human Y chromosome

JOURNAL Science 278 (5338), 675-680 (1997)

MEDLINE 98022381

REMARK SEQUENCE FROM N.A.

COMMENT -----

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[SIMILARITY] TO OTHER 'DEAD' BOX FAMILY HELICASES. BELONGS TO THE PL10 SUBFAMILY.

FEATURES Location/Qualifiers

source 1..660

/organism="Homo sapiens"
/db_xref="taxon:9606"

gene 1..660

/gene="DBY"

Protein 1..660

/gene="DBY"
/product="DEAD BOX PROTEIN 3, Y-CHROMOSOMAL"

Site 222..229

/gene="DBY"
/site_type="np-binding"
/note="ATP (POTENTIAL)."

Site 345..348

/gene="DBY"
/site_type="unclassified"
/note="DEAD BOX."

ORIGIN

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241 ytdgpgealk avkengrygr rkqypislv aptrelavqi yeearkfsyr srvrpcvvvg
301 gadigqqird lergchllva tpgrlvdme rgkigldfck ylvldeadrm ldmgfepqir
361 riveqdtmpp kgvrhtmmfs atfpkeiqml ardfldleyif lavgrvgsts enitqkvvwv
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481 alhqfrsgks pilvatavaa rgldisnvrh vinfalpsdi eeyvhriegrt grvgnlglat
541 sffneknmni tkdlldllve akqevpswle nmayehhykg gsrrgrsksnr fsoggfgardy
601 rqssgssssg fgasrgsssr sggggygdsr gfqgggyggf ynsdgyggny nsqgvdwwgn

//

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May 3 2004 07:33:01

Name: MIPS
Institution: MIPS
Address: Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

CITATIONS

Title: EST (Ottenwaelder, et al.)
Authors: Ottenwaelder,B., Obermaier,B., Mewes,H.W., Gassenhuber,J.,
Wiemann,S.
Year: 1999
Status: Unpublished

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Revision history for AL042306

GI	Version	Update Date	Status
5421648	1	Jul 8 1999 7:06 PM	Live

Accession AL042306 was first seen at NCBI on Jul 8 1999 7:06 PM

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(dT) primer [5'
TGTTACCAATCTGAAGTGGGAGCGGCCAATTTTTTTTTTTTT
3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-Merck EST Project 1997
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson,R.
Year: 1997
Status: Unpublished

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TGTTACCAATCTGAAGTGGGAGCGGCCAATTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-Merck EST Project 1997
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson,R.
Year: 1997
Status: Unpublished

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Fax: 3018699423
E-mail: arkerlav@tigr.org

CITATIONS

Medline UID: 96026280
Title: Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Authors: Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., Venter, J.C.
Citation: Nature 377 (6547 Suppl): 3-174 1995

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ORIGIN

1 cttgcttcca accctggc tc agggcg tcc aaccaggcccc ggttagcctct ggggcagact
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2821 caatgttata acatgattt catgaaacag tggagactga agccttcaa agttatttga
2881 ttttttagatc atcagacatg taatgaaaat ggttcagttt gcaatgtgag ctctgtactt
2941 ggtggatgtcaaaatgttgc cttttataat atacagattt tccttggaaa taaaagatga
3001 aacacatttc cccctaaaaa aaaaaaaaaa

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 NCBI

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GGCGCACTTGCTTCTTCGCTTCGGATAGGCATGACTGATTTT
GAGACAGACACACCTGGCTTCTTCGCTTGGATAGGCATGACTGATTTT

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Search	Nucleotide	<input type="checkbox"/>	for			Go	Clear		
				Limits	Preview/Index	History	Clipboard	Details	
Display	default	<input type="checkbox"/>	Show: 20	<input type="checkbox"/>	Send to	File	<input type="checkbox"/>	Get Subsequence	Features
<input type="checkbox"/> 1: D14859. Mus musculus mRNA...[gi:286074]									

LOCUS MUSDVH 1930 bp mRNA linear ROD 04-FEB-1999
 DEFINITION Mouse mRNA for drosophila vasa homologue, partial cds.
 ACCESSION D14859
 VERSION D14859.1 GI:286074
 KEYWORDS RNA helicase; drosophila vasa homologue.
 SOURCE Mus musculus
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1930)
 AUTHORS Noce, T.
 TITLE Direct Submission
 JOURNAL Submitted (01-APR-1993) Toshiaki Noce, Mitsubishi Kasei Institute
 of Life Sciences, Developmental Biology; 11 Minamiooya, Machida,
 Tokyo 194, Japan (Tel:0427-24-6246, Fax:0427-29-1252)
 REFERENCE 2 (bases 1 to 1930)
 AUTHORS Noce, T.
 JOURNAL Unpublished (1994)
 REFERENCE 3 (sites)
 AUTHORS Fujiwara, Y., Komiya, T., Kawabata, H., Sato, M., Fujimoto, H.,
 Furusawa, M. and Noce, T.
 TITLE Isolation of a DEAD-family protein gene that encodes a murine
 homolog of Drosophila vasa and its specific expression in germ cell
 lineage
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 91 (25), 12258-12262 (1994)
 MEDLINE 95083681
 PUBMED 7991615
 FEATURES Location/Qualifiers
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 /tissue_type="gonad, testis"
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 /protein_id="BAA03584.1"
 /db_xref="GI:286075"
 /translation="FGRGKGFGNRGFLNNKFEEGDSSGFWKESNNDCEDNQTRSRGFS
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 PAASDSGNGDTYQSRSGSGRRGGYKGLNEEVVTGSGKNSWKSETEGGESSDSQGPKVY
 I PPPPPPEDEDSIFAHYOTGINFDKYDTILVEVSGHDAPPATLTFEEANLCOTLNNTI



50CTCAGGATGGACTTGTGCTAGAAGATCGGATCCCCGGCTTTATATATATACCTCGATCT
TRCTCTATATATATATATATATATATACACACACACACACACACACACACACACACACAC
CC
CACAGAC

(35)

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1: AI217144.qf47d11.x1 Soares...[gi:3796959]

IDENTIFIERS

dbEST Id: 1988110
EST name: qf47d11.x1
GenBank Acc: AI217144
GenBank gi: 3796959

CLONE INFO

Clone Id: IMAGE:1753173 (3')
Source: NCI
Insert length: 1013
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

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TTCCAACCAGTCAGGAACATCCTGTTGAGCATCTGTCAATACTTTACTAGAGGCTGTGC
TAAATGGTTATCGATTCAAGATCAAAAAGGAAATTGCTCTGCCAGTATTCCCACAACG
ACCAGNACGCCAAT

Quality: High quality sequence stops at base: 448

Entry Created: Oct 26 1998
Last Updated: Nov 10 1998

COMMENTS

cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4_RAT Q64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: Soares_testis_NHT
Organism: Homo sapiens
Sex: male
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker

R. Site 1: Not I
R. Site 2: Eco RI
Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCAATTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

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E-mail: cgapbs-r@mail.nih.gov

CITATIONS

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Year: 1997
Status: Unpublished

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Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCCAATTTTTTTTTTT 3']. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

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E-mail: cgapbs-r@mail.nih.gov

CITATIONS

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Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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			Limits	Preview/Index	History	Clipboard	Details	
Display	default		Show: 20 	Send to	File			

□ 1: AI337133. qx83b04.x1 NCI CG...[gi:4074060]

Links

[DENTIFIERS

IBEST Id: 2120875
EST name: qx83b04.x1
GenBank Acc: AI337133
GenBank gi: 4074060

CLONE INFO

Clone Id: IMAGE:2009071 (3')
Source: NCI
DNA type: cDNA

PRIMERS

Sequencing: -40UP from Gibco
PolyA Tail: Unknown

SEQUENCE

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TGTTTGGCTTAATCCCATGACTCATCATCTACTGGATTGGAGCTTGTGAAGAAGAAA
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CTCTTGACTACCAGTGAAGCCAGGAATGTATGTAATTGCAATTCTCCAACCATG

Entry Created: Dec 29 1998
Last Updated: Dec 29 1998

COMMENTS

Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D.,
Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing
Center
Clone distribution: NCI-CGAP clone distribution information
can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

PUTATIVE ID Assigned by submitter
SW:DDX4 RAT O64060 DEAD BOX PROTEIN 4 ;

LIBRARY

Lib Name: NCI_CGAP_GC6
Organism: Homo sapiens
Tissue type: pooled germ cell tumors
Lab host: DH10B
Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker
R. Site 1: Not I
R. Site 2: Eco RI
Description: Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive

hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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Description: 1st strand cDNA was prepared from mRNA obtained from Clontech Laboratories, Inc., and primed with a Not I - oligo (dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCAATTTTTTTTTTT]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization to Cot5, and was constructed by Bento Soares and M. Fatima Bonaldo.

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CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
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Year: 1997
Status: Unpublished

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Year: 1997
Status: Unpublished

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SUBMITTER

Name: Wilson RK
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Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-NCI human EST Project
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,
S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra
,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan
,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson
,R.
Year: 1997
Status: Unpublished

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Fatima Bonaldo.

SUBMITTER

Name: Robert Strausberg, Ph.D.
E-mail: cgapbs-r@mail.nih.gov

CITATIONS

Title: National Cancer Institute, Cancer Genome Anatomy Project
(CGAP), Tumor Gene Index
Authors: NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>
Year: 1997
Status: Unpublished

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May 3 2004 07:33:01

constructed by Bento Soares and M. Fatima Bonaldo.

SUBMITTER

Name: Wilson RK
Institution: Washington University School of Medicine
Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: WashU-NCI human EST Project
Authors: Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost ,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra ,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan ,F., Theising,B., White,Y., Wylie,T., Waterston,R., Wilson ,R.
Year: 1997
Status: Unpublished

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May 3 2004 07:33:01

Institution: The Institute for Genomic Research
Address: 9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
E-mail: arkerlav@tigr.org

CITATIONS

Medline UID:

96026280

Title: Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Authors: Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S. Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pellegrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., Venter, J.C.
Citation: Nature 377 (6547 Suppl): 3-174 1995

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double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

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Address: 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
E-mail: est@watson.wustl.edu

CITATIONS

Title: The WashU-Merck EST Project
Authors: Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
, Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P.,
Wilson,R.
Year: 1995
Status: Unpublished

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[5' AACTGGAGAATTAATTAAAGATCTTTTTTTTTTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo.

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E-mail: est@watson.wustl.edu

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Year: 1995
Status: Unpublished

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